

## Search History

# SCORE Search Results Details for Application 09734329 and Search Result us-09-734-329b-2.p2n.rni.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 09734329 and Search Result us-09-734-329b-2.p2n.rni.

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GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 25, 2006, 09:19:25 ; Search time 269 Seconds  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	818.5	34.3	3471	4	US-10-094-749-1170	Sequence 1170, Ap
2	505	21.2	3289	3	US-09-620-312D-436	Sequence 436, App
3	459.5	19.3	2984	3	US-09-949-016-4299	Sequence 4299, Ap
4	453	19.0	3937	3	US-10-164-595-7	Sequence 7, Appli
5	449.5	18.9	3722	3	US-10-164-595-9	Sequence 9, Appli
6	449.5	18.9	3862	3	US-10-164-595-5	Sequence 5, Appli
7	449.5	18.9	3985	3	US-10-164-595-3	Sequence 3, Appli
8	437.5	18.4	1430	3	US-09-492-985-1	Sequence 1, Appli
9	437.5	18.4	1471	3	US-09-492-985-11	Sequence 11, Appl
10	424.5	17.8	1057	3	US-09-949-016-4554	Sequence 4554, Ap
11	418.5	17.6	1079	3	US-10-131-827-8867	Sequence 8867, Ap
12	402	16.9	4863	3	US-09-949-016-3725	Sequence 3725, Ap
13	393	16.5	4859	3	US-09-814-915A-34	Sequence 34, Appl
14	393	16.5	4859	3	US-09-949-016-168	Sequence 168, App
15	393	16.5	4859	4	US-09-880-107-1647	Sequence 1647, Ap
16	366.5	15.4	589	3	US-09-229-037-29	Sequence 29, Appl
17	366.5	15.4	589	3	US-09-478-681-29	Sequence 29, Appl
18	366.5	15.4	589	3	US-09-779-233-17	Sequence 17, Appl
19	366.5	15.4	589	3	US-09-706-243A-29	Sequence 29, Appl
20	366.5	15.4	589	3	US-09-942-087A-29	Sequence 29, Appl
21	366.5	15.4	589	4	US-09-897-844A-29	Sequence 29, Appl
22	366.5	15.4	589	4	US-10-412-105-17	Sequence 17, Appl
23	366.5	15.4	589	5	US-09-844-508-28	Sequence 28, Appl
24	366.5	15.4	589	5	US-10-245-415B-29	Sequence 29, Appl
25	360.5	15.1	1734	3	US-09-949-016-2024	Sequence 2024, Ap
26	359	15.1	298	3	US-09-229-037-14	Sequence 14, Appl
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28	359	15.1	298	3	US-09-779-233-2	Sequence 2, Appli
29	359	15.1	298	3	US-09-706-243A-14	Sequence 14, Appl
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44	351	14.7	292	3	US-09-941-450-14	Sequence 14, Appl
45	351	14.7	298	3	US-09-229-037-16	Sequence 16, Appl

# ALIGNMENTS

## RESULT 1

US-10-094-749-1170  
; Sequence 1170, Application US/10094749  
; Patent No. 6979557  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHIKO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOUYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA  
; FILE REFERENCE: 084335/0160  
; CURRENT APPLICATION NUMBER: US/10/094,749  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/350,435  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: JP 2001-328381  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 3381  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1170  
; LENGTH: 3471  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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# SCORE Search Results Details for Application 09734329 and Search Result us-09-734-329b-2.p2n.rnpbm.

<a href="#">Score Home Page</a>	<a href="#">Retrieve Application List</a>	<a href="#">SCORE System Overview</a>	<a href="#">SCORE FAQ</a>	<a href="#">Comments / Suggestions</a>
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OM protein - nucleic search, using frame\_plus\_p2n model

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#### SUMMARIES

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6	650.5	27.3	4311	13	US-11-097-143-847	Sequence 847, App
7	553.5	23.2	1830	7	US-10-312-680-1	Sequence 1, Appli
8	551.5	23.1	1197	7	US-10-312-680-3	Sequence 3, Appli
9	505	21.2	2862	8	US-10-479-435-50	Sequence 50, Appl
10	505	21.2	3024	10	US-10-888-875-1	Sequence 1, Appli
11	505	21.2	3289	6	US-10-037-270-436	Sequence 436, App
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13	505	21.2	3289	10	US-10-122-851-436	Sequence 436, App
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29	408	17.1	1615	7	US-10-264-049-704	Sequence 704, App
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; Patent No. US20020156031A1
; GENERAL INFORMATION:
; APPLICANT: de CROMBRUGGHE, BENOIT
; APPLICANT: NAKASHIMA, KAZUHISA
; APPLICANT: ZHOU, XIN
; TITLE OF INVENTION: MASTER BONE FORMATION TRANSCRIPTION FACTOR:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: UTXC:666
; CURRENT APPLICATION NUMBER: US/09/734,329
; CURRENT FILING DATE: 2000-11-30
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; NAME/KEY: CDS
; LOCATION: (100)..(1383)
US-09-734-329-1

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Comments /  
Suggestions

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# SUMMARIES

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22	438	18.4	3288	8	US-11-266-748A-28709	Sequence 28709, A
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c 26	399.5	16.8	1000	8	US-11-266-748A-342778	Sequence 342778, A
27	393.5	16.5	842	8	US-11-266-748A-363880	Sequence 363880, A
28	393.5	16.5	842	8	US-11-266-748A-388190	Sequence 388190, A
c 29	393.5	16.5	842	8	US-11-266-748A-447259	Sequence 447259, A
30	393	16.5	4859	8	US-11-266-748A-28713	Sequence 28713, A
31	392	16.4	2129	8	US-11-293-697-1978	Sequence 1978, Ap
32	371	15.6	1000	8	US-11-266-748A-403925	Sequence 403925, A
c 33	371	15.6	1000	8	US-11-266-748A-474971	Sequence 474971, A
34	370.5	15.5	1618	8	US-11-266-748A-29737	Sequence 29737, A
35	369.5	15.5	499	8	US-11-266-748A-141	Sequence 141, App
36	364.5	15.3	1152	6	US-10-511-937-402	Sequence 402, App
37	358	15.0	1668	8	US-11-266-748A-358069	Sequence 358069, A
c 38	358	15.0	1668	8	US-11-266-748A-441448	Sequence 441448, A
39	354.5	14.9	1869	8	US-11-293-697-1940	Sequence 1940, Ap
40	353.5	14.8	2639	8	US-11-235-814-2	Sequence 2, Appli
41	351.5	14.7	1953	8	US-11-266-748A-32031	Sequence 32031, A
42	346.5	14.5	1953	8	US-11-266-748A-186388	Sequence 186388, A



	43	345	14.5	2908	8	US-11-235-814-1	Sequence 1, Appli
	44	342.5	14.4	1000	8	US-11-266-748A-117354	Sequence 117354,
c	45	342.5	14.4	1000	8	US-11-266-748A-159518	Sequence 159518,

# ALIGNMENTS

## RESULT 1

US-11-266-748A-31703  
; Sequence 31703, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 31703  
; LENGTH: 3794  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-31703

## Alignment Scores:

Pred. No.:	3.09e-20	Length:	3794
Score:	674.00	Matches:	176
Percent Similarity:	49.3%	Conservative:	43
Best Local Similarity:	39.6%	Mismatches:	131
Query Match:	28.3%	Indels:	96
DB:	8	Gaps:	20

US-09-734-329B-2 (1-428) x US-11-266-748A-31703 (1-3794)

Qy	18	AlaMetLeuThrAlaAlaCysSerLysPheGlyGlySerSerProLeuArgAspSerThr	37
Db	276	GCAATGCTAACCGCTGTCTGCGGC-----	299
Qy	38	ThrLeuGlyLysGlyGlyThrLysLysProTyrAlaAspLeuSerAlaProLysThrMet	57
		:::	
Db	300	TCTCTGGGCAGCCAGCACACGGAAGCGCCGACGCCCTCCCC-GCCGCGCCTCGA-----	352

Comments /  
Suggestions

[Go Back to previous page](#)

<http://es/ScoreAccessWeb/GetItem.action?AppId=09734329&seqId=568837&ItemName=us-...> 8/1/06

2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
 9: geneseqn2003bs:\*  
 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID		Description
	1	2384	100.0	2960	6	AAD40709	Aad40709 Mouse ost
	2	2264.5	95.0	3153	13	ADR08250	Adr08250 Full leng
	3	854.5	35.8	1737	12	ADP28826	Adp28826 Human sec
c	4	836.5	35.1	3128	13	ADR07977	Adr07977 Full leng
	5	818.5	34.3	3471	10	ADA53602	Ada53602 Human cod
	6	818.5	34.3	3471	14	AEB53898	Aeb53898 DNA encod
	7	774.5	32.5	1473	12	ADO00467	Ado00467 Novel hum
	8	774.5	32.5	1473	12	ADN98898	Adn98898 Novel hum
	9	686	28.8	2076	4	ABL02405	Abl02405 Drosophil
	10	676	28.4	1675	5	AAS79321	Aas79321 DNA encod
	11	674	28.3	3794	13	ADR07645	Adr07645 Full leng
	12	671.5	28.2	1206	12	ACH87003	Ach87003 Human gen
	13	669	28.1	3846	13	ADR07511	Adr07511 Full leng
	14	650.5	27.3	4311	4	ABL02404	Abl02404 Drosophil
	15	553.5	23.2	1830	6	ABA96948	Aba96948 Mouse Spl
	16	552	23.2	1925	14	ADX83136	Adx83136 Human TEG
	17	551.5	23.1	1197	6	ABA96949	Aba96949 Human Spl
	18	551.5	23.1	1554	10	ADC30435	Adc30435 Human nov
	19	505	21.2	2862	10	AAD51694	Aad51694 Human nuc
	20	505	21.2	3024	14	ADZ72114	Adz72114 Human tra
	21	505	21.2	3289	4	AAI58549	Aai58549 Human pol
	22	505	21.2	3289	5	ADQ98766	Adq98766 DNA encod
	23	505	21.2	3289	9	ADB48526	Adb48526 Novel hum
	24	501.5	21.0	3090	4	AAI60335	Aai60335 Human pol
	25	493.5	20.7	3187	4	ABL09749	Abl09749 Drosophil
c	26	493.5	20.7	5187	4	ABL09748	Abl09748 Drosophil
	27	453	19.0	3936	14	ADZ72116	Adz72116 Human tra
	28	453	19.0	3937	10	ADK65768	Adk65768 Angiogene
	29	449.5	18.9	1848	13	ADT07445	Adt07445 Human col
	30	449.5	18.9	1923	13	ADT07444	Adt07444 Human col
	31	449.5	18.9	3312	13	ADT07441	Adt07441 Human col
	32	449.5	18.9	3430	13	ADT07439	Adt07439 Human col
	33	449.5	18.9	3448	13	ADT07440	Adt07440 Human col
	34	449.5	18.9	3548	6	ABK84634	Abk84634 Human cDN
	35	449.5	18.9	3548	14	ADX07998	Adx07998 Cyclin-de
	36	449.5	18.9	3548	15	AEF74819	Aef74819 Human pol
	37	449.5	18.9	3707	13	ADT07438	Adt07438 Human col

38	449.5	18.9	3709	8	ABX63360	Abx63360 Human cDN
39	449.5	18.9	3722	10	ADK65770	Adk65770 Angiogene
40	449.5	18.9	3763	14	AEA19695	Aea19695 Novel hum
41	449.5	18.9	3862	10	ADK65766	Adk65766 Angiogene
42	449.5	18.9	3920	13	ADR83463	Adr83463 Human Sp3
43	449.5	18.9	3985	10	ADK65764	Adk65764 Angiogene
44	438	18.4	2888	15	AEe80965	Aee80965 Human cDN
45	438	18.4	3288	6	ABK83634	Abk83634 Human cDN

# ALIGNMENTS

## RESULT 1

AAD40709

ID AAD40709 standard; cDNA; 2960 BP.

XX

AC AAD40709;

XX

DT 30-OCT-2002 (first entry)

XX

DE Mouse osterix cDNA.

XX

KW Bone formation; transcription factor; osteoblast; Paget's disease;  
KW osterix protein; glucocorticoid; osteoporosis; cytostatic; cytokine;  
KW periodontal disease; tooth loss; bone fracture; rheumatoid arthritis;  
KW metastatic bone disease; gene therapy; growth factor; osteopathic;  
KW differentiation; mouse; chromosome 15; gene; ss.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT CDS 100. .1386

FT /\*tag= a

FT /product= "Mouse osterix protein"

XX

PN WO200244380-A2.

XX

PD 06-JUN-2002.

XX

PF 30-NOV-2001; 2001WO-US044898.

XX

PR 30-NOV-2000; 2000US-00734329.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI De Crombrugghe B, Nakashima K, Zhou X;

XX

DR WPI; 2002-519587/55.

DR P-PSDB; AAE25076.

XX

PT Novel DNA segment encoding Osterix polypeptide which is a master  
PT transcription factor that controls osteoblast differentiation and is  
PT useful for treating osteoporosis, in patient by stimulating bone  
PT formation.

XX

PS Claim 17; Page 138-141; 144pp; English.

XX

CC The invention relates to a master bone formation transcription factor  
CC that controls osteoblast differentiation, osterix protein and its  
CC corresponding nucleic acid sequence. Osterix protein and its DNA and  
CC agents that interact with the protein to activate or stimulate the



Qy	181	ThrGlyProAlaGlnProProLeuAsnProGlnLeuProThrTyrProSerAspPheAla	200
Db	640	ACAGGCCCTGCCAGCCTCCACTGAACCCCCAGCTGCCTACTTACCCATCTGACTTTGCT	699
Qy	201	ProLeuAsnProAlaProTyrProAlaProHisLeuLeuGlnProGlyProGlnHisVal	220
Db	700	CCCCTTAACCCAGCTCCCTACCCAGCGCCCCACCTCTTGCAACCAGGGCCCCAGCATGTC	759
Qy	221	LeuProGlnAspValTyrLysProLysAlaValGlyAsnSerGlyGlnLeuGluGlySer	240
Db	760	CTACCCCAAGATGTCCTATAAGCCCAAGGCGGTTGGCAATAGTGGGCAACTGGAGGGGAGT	819
Qy	241	GlyAlaAlaLysProProArgGlyAlaGlyThrGlyGlySerGlyGlyTyrAlaGlySer	260
Db	820	GGTGCAGCCAAACCCCTCGGGGTGCTGGCACAGGGGGCAGCGGTGGATATGCGGGCAGT	879
Qy	261	GlyAlaGlyArgSerThrCysAspCysProAsnCysGlnGluLeuGluArgLeuGlyAla	280
Db	880	GGGGCAGGGCGTTCTACCTGCGACTGCCCAACTGTCAGGAGCTAGAGCGGCTCGGGGCA	939
Qy	281	AlaAlaAlaGlyLeuArgLysLysProIleHisSerCysHisIleProGlyCysGlyLys	300
Db	940	GCAGCGGCTGGGCTGAGGAAGAAGCCCATTACAGCTGCCACATCCCTGGGTGCGGCAAG	999
Qy	301	ValTyrGlyLysAlaSerHisLeuLysAlaHisLeuArgTrpHisThrGlyGluArgPro	320
Db	1000	GTGTACGGCAAGGCTTCGCATCTGAAAGCCCACTTGCGCTGGCACACTGGCGAGAGGCCT	1059
Qy	321	PheValCysAsnTrpLeuPheCysGlyLysArgPheThrArgSerAspGluLeuGluArg	340
Db	1060	TTCGTCTGCAACTGGCTTTTCTGCGGCAAGAGGTTCACTCGCTCTGACGAGCTGGAGCGC	1119
Qy	341	HisValArgThrHisThrArgGluLysLysPheThrCysLeuLeuCysSerLysArgPhe	360
Db	1120	CACGTGCGCACTCACACCCGGGAGAAGAAGTTCACTTGCTTGCTCTGTTCCAAGCGCTTT	1179
Qy	361	ThrArgSerAspHisLeuSerLysHisGlnArgThrHisGlyGluProGlyProGlyPro	380
Db	1180	ACCAGAAGCGACCACTTGAGCAAACATCAGCGCACCCACGGGGAGCCAGGCCCGGGACCG	1239
Qy	381	ProProSerGlyProLysGluLeuGlyGluGlyArgSerValGlyGluGluGluAlaAsn	400
Db	1240	CCCCAAGTGCCCTAAGGAGCTGGGGGAGGGTCGCAGCGTCGGGGAAGAAGAAGCCAAT	1299
Qy	401	GlnProProArgSerSerThrSerProAlaProProGluLysAlaHisGlyGlySerPro	420
Db	1300	CAGCCGCCCCGATCTTCCACTTCGCCTGCACCCCCAGAAAAAGCCACGGAGGCAGCCCA	1359
Qy	421	GluGlnSerAsnLeuLeuGluIle	428
Db	1360	GAGCAGAGCAACCTGCTAGAGATC	1383

RESULT 2

ADR08250

ID ADR08250 standard; cDNA; 3153 BP.

XX

AC ADR08250;

XX

DT 04-NOV-2004 (first entry)

XX

# SCORE Search Results Details for Application 09734329 and Search Result us-09-734-329b-2.p2n.rge.

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GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 25, 2006, 09:19:19 ; Search time 10184 Seconds  
(without alignments)  
4031.249 Million cell updates/sec

Title: US-09-734-329B-2  
Perfect score: 2384  
Sequence: 1 MASSLLEEEAHYGSSPLAML.....PAPPEKAHGGSP EQSNLLEI 428

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US09734329/runat_25072006_091902_3663/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US09734329 @CGN_1_1_8328 @runat_25072006_091902_3663 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : GenEmbl:\*  
1: gb\_env:\*

2: gb\_pat:\*  
 3: gb\_ph:\*  
 4: gb\_pl:\*  
 5: gb\_pr:\*  
 6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%		Query		DB	ID	Description
	No.	Score	Match	Length			
	1	2384	100.0	2284	6	BC113150	BC113150 Mus muscu
	2	2384	100.0	2960	2	AX555029	AX555029 Sequence
	3	2384	100.0	2960	6	AF184902	AF184902 Mus muscu
c	4	2360	99.0	138860	12	AC055703	AC055703 Mus muscu
c	5	2360	99.0	205599	6	AC137156	AC137156 Mus muscu
c	6	2360	99.0	208289	6	AC163291	AC163291 Mus muscu
	7	2356	98.8	1403	6	AY803733	AY803733 Mus muscu
	8	2338	98.1	1287	6	AY177399	AY177399 Rattus no
c	9	2333	97.9	254686	12	AC097309	AC097309 Rattus no
	10	2264.5	95.0	1357	5	BC101549	BC101549 Homo sapi
	11	2264.5	95.0	2843	5	AY150673	AY150673 Homo sapi
	12	2264.5	95.0	2971	5	AF466179	AF466179 Homo sapi
	13	2264.5	95.0	2995	5	AF477981	AF477981 Homo sapi
	14	2264.5	95.0	3153	2	CQ851287	CQ851287 Sequence
	15	2264.5	95.0	3153	5	AK128520	AK128520 Homo sapi
	16	2240.5	94.0	1575	2	CQ740107	CQ740107 Sequence
c	17	2239.5	93.9	106551	5	AC073611	AC073611 Homo sapi
	18	2239.5	93.9	166697	12	AC021103	AC021103 Homo sapi
	19	2236.5	93.8	1350	5	AY150674	AY150674 Homo sapi
	20	2212.5	92.8	173487	12	AC166700	AC166700 Bos tauru
	21	1301	54.6	1433	11	AY380818	AY380818 Danio rer
	22	866.5	36.3	2381	11	AY769697	AY769697 Danio rer
	23	857.5	36.0	1940	11	BC067673	BC067673 Danio rer
	24	857.5	36.0	1977	11	AY731230	AY731230 Danio rer
	25	854.5	35.8	2380	6	AY591908	AY591908 Mus muscu
	26	843	35.4	1765	11	AY769696	AY769696 Danio rer
	27	842.5	35.3	2459	11	AY591905	AY591905 Danio rer
	28	842.5	35.3	240532	12	AC130082	AC130082 Rattus no
	29	838.5	35.2	2382	11	BC067654	BC067654 Danio rer
c	30	836.5	35.1	3128	2	CQ851014	CQ851014 Sequence
c	31	836.5	35.1	3128	5	AK128215	AK128215 Homo sapi
	32	836.5	35.1	171734	6	AL954713	AL954713 Mouse DNA
	33	836.5	35.1	174437	5	AC018470	AC018470 Homo sapi
	34	836.5	35.1	211696	12	AC099580	AC099580 Mus muscu
	35	833	34.9	2053	11	AY591904	AY591904 Danio rer
	36	829	34.8	155001	11	BX005032	BX005032 Zebrafish
	37	828.5	34.8	1618	5	AY167047	AY167047 Homo sapi



38	823	34.5	1747	11	BC065597	BC065597 Danio rer
39	822.5	34.5	2919	11	AY457141	AY457141 Danio rer
40	818.5	34.3	3471	2	AX714486	AX714486 Sequence
41	818.5	34.3	3471	5	AK056857	AK056857 Homo sapi
42	815.5	34.2	190372	6	AC131717	AC131717 Mus muscu
43	815.5	34.2	191231	6	AC126277	AC126277 Mus muscu
44	811.5	34.0	3581	5	BC038669	BC038669 Homo sapi
45	810.5	34.0	1606	5	AY167048	AY167048 Homo sapi

# ALIGNMENTS

## RESULT 1

BC113150

LOCUS BC113150 2284 bp mRNA linear ROD 06-FEB-2006

DEFINITION Mus musculus trans-acting transcription factor 7, mRNA (cDNA clone MGC:130562 IMAGE:40054399), complete cds.

ACCESSION BC113150

VERSION BC113150.1 GI:86577831

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2284)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRMT Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 2284)

AUTHORS .

CONSRMT NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (05-FEB-2006) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Baylor Human Genome Sequencing Center

cDNA Library Preparation: Baylor Human Genome Sequencing Center

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAM Plate: 15 Row: f Column: 19.

FEATURES	Location/Qualifiers
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gene	1. .2284 /gene="Sp7" /note="synonym: C22" /db_xref="GeneID:170574" /db_xref="MGI:2153568"
CDS	38. .1324 /gene="Sp7" /codon_start=1 /product="Sp7 protein" /protein_id="AAI13151.1" /db_xref="GI:86577832" /db_xref="GeneID:170574" /db_xref="MGI:2153568" /translation="MASSLLEEEAHYGSS PLAMLTAACSKFGGSS PLRDSTTLGKGGT KKPYADLSAPKTMGDYAPAFSSSTNGLLS PAGSPAPASGYANDY PPFPHSFPGP TGA QDPGLLVPKGHSSSDCLPSVYTS LDMTHPYGSWYKAGIHAGISPGPGNTPT PWDMHP GGNWLGGGQGGDGLQGTLSGPAQPPLNPQLPTYP SDFAPLNPAPYP APHLLQPGPQ HVL PQDVYKPKAVGN SGQLEGSGAAKPPRGAGTGGSGGYAGS GAGRSTCDCPNCQELE RLGAAAAGLRKKPIHSCHIPGCGKVY GKASHLKAHLR WHTGERPFVCNWLFCGKRFT R SDELERHVRTH TREKKFTCLLC SKRFT RSDHLSKHQ RTHGEPGPGPPPSGPKELGEGR SVGEEANQPPRSSTSPAPPE KAHGGSP EQSNLLEI"

#### ORIGIN

#### Alignment Scores:

Pred. No.:	3.49e-131	Length:	2284
Score:	2384.00	Matches:	428
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-734-329B-2 (1-428) x BC113150 (1-2284)

Qy 1 MetAlaSerSerLeuLeuGluGluGluAlaHisTyrGlySerSerProLeuAlaMetLeu 20

Db	38		ATGGCGTCCTCTCTGCTTGAGGAAGAAGCTCACTATGGCTCCAGTCCCCTGGCCATGCTG	97
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Qy	41		LysGlyGlyThrLysLysProTyrAlaAspLeuSerAlaProLysThrMetGlyAspAla	60
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Qy	81		ProAlaSerGlyTyrAlaAsnAspTyrProProPheProHisSerPheProGlyProThr	100
Db	278		CCAGCCTCTGGCTATGCAAATGACTACCCACCCTTCCCTCACTCATTTCTGGGCCCCACC	337
Qy	101		GlyAlaGlnAspProGlyLeuLeuValProLysGlyHisSerSerSerAspCysLeuPro	120
Db	338		GGTGCCCAAGACCCTGGGCTCCTAGTGCCTAAGGGGCACAGCTCGTCTGACTGCCTGCCT	397
Qy	121		SerValTyrThrSerLeuAspMetThrHisProTyrGlySerTrpTyrLysAlaGlyIle	140
Db	398		AGTGTCTACACTTCCTGGATATGACTCATCCCTATGGCTCGTGGTACAAGGCAGGCATC	457
Qy	141		HisAlaGlyIleSerProGlyProGlyAsnThrProThrProTrpTrpAspMetHisPro	160
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Qy	161		GlyGlyAsnTrpLeuGlyGlyGlyGlnGlyGlnGlyAspGlyLeuGlnGlyThrLeuSer	180
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Qy	181		ThrGlyProAlaGlnProProLeuAsnProGlnLeuProThrTyrProSerAspPheAla	200
Db	578		ACAGGCCCTGCCAGCCTCCACTGAACCCCCAGCTGCCTACTTACCCATCTGACTTTGCT	637
Qy	201		ProLeuAsnProAlaProTyrProAlaProHisLeuLeuGlnProGlyProGlnHisVal	220
Db	638		CCCCTTAACCCAGCTCCCTACCCAGCGCCCCACCTCTTGCAACCAGGGCCCCAGCATGTC	697
Qy	221		LeuProGlnAspValTyrLysProLysAlaValGlyAsnSerGlyGlnLeuGluGlySer	240
Db	698		CTACCCCAAGATGTCTATAAGCCCAAGGCGGTGGCAATAGTGGGCAACTGGAGGGGAGT	757
Qy	241		GlyAlaAlaLysProProArgGlyAlaGlyThrGlyGlySerGlyGlyTyrAlaGlySer	260
Db	758		GGTGCAGCCAAACCCCTCGGGGTGCTGGCACAGGGGGCAGCGGTGATATGCGGGCAGT	817
Qy	261		GlyAlaGlyArgSerThrCysAspCysProAsnCysGlnGluLeuGluArgLeuGlyAla	280
Db	818		GGGGCAGGGCGTTCTACCTGCGACTGCCCAACTGTCAGGAGCTAGAGCGGCTCGGGGCA	877
Qy	281		AlaAlaAlaGlyLeuArgLysLysProIleHisSerCysHisIleProGlyCysGlyLys	300
Db	878		GCAGCGGCTGGGCTGAGGAAGAAGCCCATTCACAGCTGCCACATCCCTGGGTGCGGCAAG	937
Qy	301		ValTyrGlyLysAlaSerHisLeuLysAlaHisLeuArgTrpHisThrGlyGluArgPro	320

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Qy 361 ThrArgSerAspHisLeuSerLysHisGlnArgThrHisGlyGluProGlyProGlyPro 380  
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RESULT 2

AX555029

LOCUS AX555029 2960 bp DNA linear PAT 27-NOV-2002

DEFINITION Sequence 1 from Patent WO0244380.

ACCESSION AX555029

VERSION AX555029.1 GI:25898589

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS de Crombrughe,B., Nakashima,K. and Zhou,X.

TITLE Master bone formation transcription factor: compositions and  
 methods of use

JOURNAL Patent: WO 0244380-A 1 06-JUN-2002;

BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)

FEATURES Location/Qualifiers

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CDS 100. .1386

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ORIGIN

Alignment Scores:

Pred. No.:	4.78e-131	Length:	2960
Score:	2384.00	Matches:	428
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-09-734-329B-2 (1-428) x AX555029 (1-2960)

Qy	1	MetAlaSerSerLeuLeuGluGluGluAlaHisTyrGlySerSerProLeuAlaMetLeu	20
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Qy	21	ThrAlaAlaCysSerLysPheGlyGlySerSerProLeuArgAspSerThrThrLeuGly	40
Db	160	ACTGCAGCCTGCAGCAAATTTGGCGGCTCTAGCCCTCTGCGGGACTCAACAACCCTGGGG	219
Qy	41	LysGlyGlyThrLysLysProTyrAlaAspLeuSerAlaProLysThrMetGlyAspAla	60
Db	220	AAAGGAGGCACAAAGAAGCCATACGCTGACCTTTTCAGCCCCAAAACCATGGGGGACGCC	279
Qy	61	TyrProAlaProPheSerSerThrAsnGlyLeuLeuSerProAlaGlySerProProAla	80
Db	280	TACCCAGCTCCCTTCTCAAGCACCAATGGACTCCTCTCTCCTGCAGGCAGTCTCCGGCC	339
Qy	81	ProAlaSerGlyTyrAlaAsnAspTyrProProPheProHisSerPheProGlyProThr	100
Db	340	CCAGCCTCTGGCTATGCAAATGACTACCCACCCTTCCTCACTCATTTCTGGGCCCACC	399
Qy	101	GlyAlaGlnAspProGlyLeuLeuValProLysGlyHisSerSerSerAspCysLeuPro	120
Db	400	GGTGGCCAAGACCCTGGGCTCCTAGTGCCTAAGGGGCACAGCTCGTCTGACTGCCTGCCT	459
Qy	121	SerValTyrThrSerLeuAspMetThrHisProTyrGlySerTrpTyrLysAlaGlyIle	140
Db	460	AGTGTCTACACTTCCCTGGATATGACTCATCCCTATGGCTCGTGGTACAAGGCAGGCATC	519
Qy	141	HisAlaGlyIleSerProGlyProGlyAsnThrProThrProTrpTrpAspMetHisPro	160
Db	520	CACGCAGGCATCTCACCAGGTCCAGGCAACACACCTACTCCTTGGTGGGACATGCACCCT	579
Qy	161	GlyGlyAsnTrpLeuGlyGlyGlyGlnGlyGlnGlyAspGlyLeuGlnGlyThrLeuSer	180
Db	580	GGGGGCAACTGGCTAGGTGGTGGTCAAGGGCCAGGGTGATGGGCTGCAAGGGACACTGTCC	639
Qy	181	ThrGlyProAlaGlnProProLeuAsnProGlnLeuProThrTyrProSerAspPheAla	200
Db	640	ACAGGCCCTGCCCAGCCTCCACTGAACCCCAGCTGCCTACTTACCCATCTGACTTTGCT	699
Qy	201	ProLeuAsnProAlaProTyrProAlaProHisLeuLeuGlnProGlyProGlnHisVal	220
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RESULT 3

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AF184902
LOCUS      AF184902                2960 bp    mRNA    linear    ROD 12-JAN-2002
DEFINITION Mus musculus Osterix (C22) mRNA, complete cds.
ACCESSION  AF184902
VERSION    AF184902.1  GI:18138080
KEYWORDS   .
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 2960)
AUTHORS    Nakashima,K., Zhou,X., Kunkel,G., Zhang,Z., Deng,J.M.,
            Behringer,R.R. and de Crombrughe,B.
TITLE      The novel zinc finger-containing transcription factor osterix is
            required for osteoblast differentiation and bone formation
JOURNAL    Cell 108 (1), 17-29 (2002)
PUBMED     11792318
REFERENCE  2 (bases 1 to 2960)
AUTHORS    Nakashima,K., Zhou,X. and de Crombrughe,B.

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TITLE Direct Submission  
JOURNAL Submitted (10-SEP-1999) Molecular Genetics, M.D. Anderson Cancer Center, 1515 Holcombe, Houston, TX 77030, USA

FEATURES Location/Qualifiers  
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# ORIGIN

## Alignment Scores:

Pred. No.:	4.78e-131	Length:	2960
Score:	2384.00	Matches:	428
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-734-329B-2 (1-428) x AF184902 (1-2960)

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Qy	41	LysGlyGlyThrLysLysProTyrAlaAspLeuSerAlaProLysThrMetGlyAspAla	60
Db	220	AAAGGAGGCACAAAGAAGCCATACGCTGACCTTTCAGCCCCAAACCATGGGGGACGCC	279
Qy	61	TyrProAlaProPheSerSerThrAsnGlyLeuLeuSerProAlaGlySerProProAla	80
Db	280	TACCCAGCTCCCTTCTCAAGCACCAATGGACTCCTCTCTCCTGCAGGCAGTCTCCGGCC	339
Qy	81	ProAlaSerGlyTyrAlaAsnAspTyrProProPheProHisSerPheProGlyProThr	100
Db	340	CCAGCCTCTGGCTATGCAAATGACTACCCACCCTTCCCTCACTCATTTCTGGGGCCACC	399
Qy	101	GlyAlaGlnAspProGlyLeuLeuValProLysGlyHisSerSerSerAspCysLeuPro	120

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Db	460		AGTGTCTACACTTCCTGGATATGACTCATCCCTATGGCTCGTGGTACAAGGCAGGCATC	519
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Qy	161		GlyGlyAsnTrpLeuGlyGlyGlyGlnGlyGlnGlyAspGlyLeuGlnGlyThrLeuSer	180
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Db	640		ACAGGCCCTGCCAGCCTCCACTGAACCCCCAGCTGCCTACTTACCCATCTGACTTTGCT	699
Qy	201		ProLeuAsnProAlaProTyrProAlaProHisLeuLeuGlnProGlyProGlnHisVal	220
Db	700		CCCCTTAACCCAGCTCCCTACCCAGCGCCCCACCTCTTGCAACCAGGGCCCCAGCATGTC	759
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Qy	241		GlyAlaAlaLysProProArgGlyAlaGlyThrGlyGlySerGlyGlyTyrAlaGlySer	260
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Qy	281		AlaAlaAlaGlyLeuArgLysLysProIleHisSerCysHisIleProGlyCysGlyLys	300
Db	940		GCAGCGGCTGGGCTGAGGAAGAAGCCATTACAGCTGCCACATCCCTGGGTGCGGCAAG	999
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Qy	341		HisValArgThrHisThrArgGluLysLysPheThrCysLeuLeuCysSerLysArgPhe	360
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Qy	361		ThrArgSerAspHisLeuSerLysHisGlnArgThrHisGlyGluProGlyProGlyPro	380
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Qy	381		ProProSerGlyProLysGluLeuGlyGluGlyArgSerValGlyGluGluGluAlaAsn	400
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RESULT 4

AC055703/c

LOCUS AC055703 138860 bp DNA linear HTG 15-MAY-2002

DEFINITION Mus musculus strain C57BL6/J clone RP23-399N14, WORKING DRAFT  
 SEQUENCE, 37 unordered pieces.

ACCESSION AC055703

VERSION AC055703.9 GI:20279384

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 138860)

AUTHORS Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,  
 Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,  
 Gordon,M., Goltz,J.S. and Kucherlapati,R.

TITLE High Throughput Mouse Sequencing

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 138860)

AUTHORS Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,  
 Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,  
 Gordon,M., Goltz,J.S. and Kucherlapati,R.

TITLE Direct Submission

JOURNAL Submitted (18-APR-2000) Department of Molecular Genetics, Albert  
 Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,  
 Bronx, NY 10461, USA

REFERENCE 3 (bases 1 to 138860)

AUTHORS Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,  
 Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,  
 Gordon,M., Goltz,J.S. and Kucherlapati,R.

TITLE Direct Submission

JOURNAL Submitted (24-APR-2002) Harvard Partners Center for Genetics and  
 Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA  
 02139, USA

COMMENT On Apr 24, 2002 this sequence version replaced gi:18151001.

-----Genome Center

Center: Harvard Partners Genome Center

Center Code: HPGC

Web site: <http://www.hpcgg.org/Sequence/mouse.html>

Contact: [hpgc@mendel.mgh.harvard.edu](mailto:hpgc@mendel.mgh.harvard.edu)

-----Summary Statistics

Center project name: AAS

Sequencing vector: pUC18; L08752

Chemistry: Dye-terminator Big Dye; 100%

\*Consensus quality: 126666 at least Q20

\*Consensus quality: 122952 at least Q30

\*Consensus quality: 116499 at least Q40

Estimated insert size: agarose-FP - N/A

\*\*Estimated insert size: 138140 - sum-of-contigs

Quality coverage: agarose-FP - N/A

Quality coverage: 9.1 x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 37 contigs. The true order of the pieces

Comments /  
Suggestions

[Go Back to previous page](#)

<http://es/ScoreAccessWeb/GetItem.action?AppId=09734329&seqId=568843&ItemName=us-...> 8/1/06

2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2384	100.0	2907	6	AK032521	AK032521 Mus muscu
2	2350	98.6	2874	6	AK077375	AK077375 Mus muscu
3	2326	97.6	2917	6	AK076229	AK076229 Mus muscu
4	1182.5	49.6	938	4	BX369746	BX369746 BX369746
5	1119.5	47.0	1014	4	BX394280	BX394280 BX394280
6	1115	46.8	632	5	CF905412	CF905412 A0434B03-
7	1115	46.8	656	5	CF905401	CF905401 A0434A03-
8	1100	46.1	608	5	CF906401	CF906401 A0446H03-
9	1037.5	43.5	745	8	CN287220	CN287220 170005325
10	1000	41.9	615	7	BB622399	BB622399 BB622399
11	808.5	33.9	4301	6	AK030745	AK030745 Mus muscu
12	807.5	33.9	3659	6	AK053093	AK053093 Mus muscu
13	799	33.5	2590	6	AK135123	AK135123 Mus muscu
c 14	754.5	31.6	1798	6	BC023224	BC023224 Mus muscu
15	747.5	31.4	643	7	BB622895	BB622895 BB622895
16	704	29.5	670	7	BB618195	BB618195 BB618195
17	690	28.9	1141	10	DW031048	DW031048 CFW209-B0
c 18	672.5	28.2	5272	6	AK029830	AK029830 Mus muscu
19	667.5	28.0	1131	14	DQ047750	DQ047750 Homo sapi
20	662.5	27.8	1131	14	DQ047751	DQ047751 Pan trogl
21	662	27.8	3599	6	AK137686	AK137686 Mus muscu
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25	612.5	25.7	819	5	CK143124	CK143124 AGENCOURT
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28	588.5	24.7	561	3	BQ419249	BQ419249 faa36e03.
c 29	587	24.6	638	1	AL662349	AL662349 AL662349
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31	576	24.2	2078	3	BP525450	BP525450 BP525450
c 32	572	24.0	641	10	DT247674	DT247674 JGI_CAAU2
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35	557.5	23.4	443	1	AL960681	AL960681 AL960681
36	555.5	23.3	474	2	BI979366	BI979366 ft86e04.y
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38	552	23.2	471	12	CE281682	CE281682 tigr-gss-

c	39	517	21.7	686	10	DW253992	DW253992 UI-S-GB1-
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	41	509	21.4	1084	10	DW665599	DW665599 CNB332-C0
	42	506	21.2	899	5	CD757648	CD757648 AGENCOURT
c	43	504	21.1	694	10	DW271862	DW271862 UI-S-GS1-
	44	504	21.1	866	5	CD755971	CD755971 AGENCOURT
	45	503	21.1	836	5	CD756314	CD756314 AGENCOURT

# ALIGNMENTS

## RESULT 1

AK032521

LOCUS AK032521 2907 bp mRNA linear HTC 02-SEP-2005

DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430578P22 product:osterix, full insert sequence.

ACCESSION AK032521

VERSION AK032521.1 GI:26328334

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

PUBMED 10349636

## REFERENCE

2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 11042159

## REFERENCE

3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

## REFERENCE

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

## REFERENCE

5

AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

## REFERENCE

6

AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group  
(Genome Network Core Team) and the FANTOM Consortium.

TITLE Antisense Transcription in the Mammalian Transcriptome

JOURNAL Science 309, 1564-1566 (2005)

REFERENCE 7

AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and  
Genome Science Group (Genome Network Project Core Group).

TITLE The Transcriptional Landscape of the Mammalian Genome

JOURNAL Science 309, 1559-1563 (2005)

REFERENCE 8 (bases 1 to 2907)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,  
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-734-329B-2 (1-428) x AK032521 (1-2907)

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Qy	21	ThrAlaAlaCysSerLysPheGlyGlySerSerProLeuArgAspSerThrThrLeuGly	40
Db	153	ACTGCAGCCTGCAGCAAATTTGGCGGCTCTAGCCCTCTGCGGGACTCAACAACCCTGGGG	212
Qy	41	LysGlyGlyThrLysLysProTyrAlaAspLeuSerAlaProLysThrMetGlyAspAla	60
Db	213	AAAGGAGGCACAAAGAAGCCATACGCTGACCTTTCAGCCCCCAAACCATGGGGGACGCC	272
Qy	61	TyrProAlaProPheSerSerThrAsnGlyLeuLeuSerProAlaGlySerProProAla	80
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Qy	321		PheValCysAsnTrpLeuPheCysGlyLysArgPheThrArgSerAspGluLeuGluArg	340
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Qy	341		HisValArgThrHisThrArgGluLysLysPheThrCysLeuLeuCysSerLysArgPhe	360
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Qy	381		ProProSerGlyProLysGluLeuGlyGluGlyArgSerValGlyGluGluGluAlaAsn	400
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Qy	401		GlnProProArgSerSerThrSerProAlaProProGluLysAlaHisGlyGlySerPro	420
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Db	1353		GAGCAGAGCAACCTGCTAGAGATC	1376

RESULT 2

AK077375

LOCUS AK077375 2874 bp mRNA linear HTC 02-SEP-2005

DEFINITION Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430403B13 product:osterix, full insert sequence.

ACCESSION AK077375

VERSION AK077375.1 GI:26346245

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1